

XM_012175446.4	TCAAGAGGTAATGTTCTCACCATCCAAGTTAAAGGACCAACCCAGAATTCAAGAAGCG	60
H	TCAAGAGGTAATGTTCTCACCATCCAAGTTAAAGGACCAACCCAGAATTCAAGAAGCG	60
E	TCAAGAGGTAATGTTCTCACCATCCAAGTTAAAGGACCAACCCAGAATTCAAGAAGCG	60

XM_012175446.4	GACCACAGTGTGGTTAAAAATGAAGAGAGCCTGGTCTTTGTCCAGACAGACAAACCCAT	120
H	GACCACAGTGTGGTTAAAAATGAAGAGAGCCTGGTCTTTGTCCAGACAGACAAACCCAT	120
E	GACCACAGTGTGGTTAAAAATGAAGAGAGCCTAGTCTTTGTCCAGACAGACAAACCCAT	120

XM_012175446.4	CTATAAACAGAGCAGACAGTGAATTTTCGTATTGTCTTGTGAATGAAAGCTTTACCCC	180
H	CTATAAACAGAGCAGACAGTGAATTTTCGTATTGTCTTGTGAATGAAAGCTTTACCCC	180
E	CTATAAACAGAGCAGACAGTGAATTTTCGTATTGTCTTGTGAATGAAAGCTTTACCCC	180

XM_012175446.4	CCTGAATGAGTTGGTTCCACTAGTATATATTGAGGACCCCAAGGAAATCGCATCGCACA	240
H	CCTGAATGAGTTGGTTCCACTAGTATATATTGAGGACCCCAAGGAAATCGCATCGCACA	240
E	CCTGAATGAGTTGGTTCCACTAGTATATATTGAGGACCCCAAGGAAATCGCATCGCACA	240

XM_012175446.4	GTGGCAGAACCTCGAGGTAGAGAATGGCCTCCAGCAGTTGACCTTCCCCCTCTCGTCAGA	300
H	GTGGCAGAACCTCGAGGTAGAGAATGGCCTCCAGCAGTTGACCTTCCCCCTCTCGTCAGA	300
E	GTGGCAGAACCTCGAGGTAGAGAATGGCCTCCAGCAGTTGACCTTCCCCCTCTCGTCAGA	300

XM_012175446.4	ACCCTTTCAAGGGTCCTATAAGGTGGTGGTACAGAAAGAATCAGGTGGGACTGCAGAGCA	360
H	ACCCTTTCAAGGGTCCTATAAGGTGGTGGTACAGAAAGAATCAGGTGGGACTGCAGAGCA	360
E	ACCCTTTCAAGGGTCCTATAAGGTGGTGGTACAGAAAGAATCAGGTGGGACTGCAGAGCA	360

XM_012175446.4	CCACTTCACCGTGGAGGAATTTGTGCTTCCTAAGTTTGAAGTACAAGTAAGAATGCCAAA	420
H	CCACTTCACCGTGGAGGAATTTGTGCTTCCTAAGTTTGAAGTACAAGTAAGAATGCCAAA	420
E	CCACTTCACCGTGGAGGAATTTGTGCTTCCTAAGTTTGAAGTACAAGTAAGAATGCCAAA	420

XM_012175446.4	GACAATCACCATCTTGAAGAAGAGGTG	448
H	GACAATCACCATCTTGAAGAAGAGGTG	448
E	GACAATCACCATCTTGAAGAAGAGGTG	448

Figure S1. A2M marker (448-bp) sequences and GenBank gb|XM_012175446.4| for analyzing nitrogenous bases alignment for DNA in healthy and endometritis ewes.

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DQ890157.1  CACCTGAGGAATCTTGAATATTTGGACTTATCCTATAATCGCTTATCTAACTTATCATCT 60
H           CACCTGAGGAATCTTGAATATTTGGACTTATCCTATAATCGCTTATCTAACTTATCATCT 60
E           CACCTGAGGAATCTTGAATATTTGGACTTATCCTATAATCGCTTATCTAACTTATCATCT 60
            *****

DQ890157.1  TCCTGGTTCAGGTCCCTTTATGTCTTGAAATTCTTAACTTACTGGGAAATTTATACAAA 120
H           TCCTGGTTCAGGTCCCTTTATGTCTTGAAATTCTTAACTTACTGGGAAATTTATACAAA 120
E           TCCTGGTTCAGGTCCCTTTATGTCTTGAAATTCTTAACTTACTGGGAAATTTATACAAA 120
            *****

DQ890157.1  ACACTTGGGGAAACATCTCTTTTTTCTCATCTCCCAAATCTGCGGACCCCTGAAAGTAGGA 180
H           ACACTTGGGGAAACATCTCTTTTTTCTCATCTCCCAAATCTGCGGACCCCTGAAAGTAGGA 180
E           ACACTTGGGGAAACATCTCTTTTTTCTCATCTCCCAAATCTGCGGACCCCTGAAAGTAGGA 180
            *****

DQ890157.1  AATAGTAACAGCTTCAGTCAGATTCATGAAAAGGATTTCACTGGACTGACTTTTCTTGAG 240
H           AATAGTAACAGCTTCAGTCAGATTCATGAAAAGGATTTCACTGGACTGACTTTTCTTGAG 240
E           AATAGTAACAGCTTCAGTCAGATTCATGAAAAGGATTTCACTGGACTGACTTTTCTTGAG 240
            *****

DQ890157.1  GAGCTTGAGATCAGTGCTCAAAATCTGCAGTTGTATGTGCCAAAGAGTTTAAAGTCGATC 300
H           GAGCTTGAGATCAGTGCTCAAAATCTGCAGTTGTATGTGCCAAAGAGTTTAAAGTCGATC 300
E           GAGCTTGAGATCAGTGCTCAAAATCTGCAGTTGTATGTGCCAAAGAGTTTAAAGTCGATC 300
            *****

DQ890157.1  CAGAACATTAGCCATCTGATTCTGCATCTGAGGCAGCCTG  340
H           CAGAACATTAGCCATCTGATTCTGCATCTGAGGCAGCCTG  340
E           CAGAACATTAGCCATCTGATTCTGCATCTGAGGCAGCCTG  340
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Figure S2. *TLR2* marker (340-bp) sequences and GenBank gb|DQ890157.1| for analyzing nitrogenous bases alignment for DNA in healthy and endometritis ewes.

NM_001009400.2	CTGACGCCTGGCCGGCCGGTCCGCCGACTGTCCACCTGCAAGACCATCGACATGGAGCTG	60
H	CTGACGCCTGGCCGGCCGGTCCGCCGACTGTCCACCTGCAAGACCATCGACATGGAGCTG	60
E	CTGACGCCTGGCCGGCCGGTCCGCCGACTGTCCACCTGCAAGACCATCGACATGGAGCTG	60

NM_001009400.2	GTGAAGCGGAAGGGCATCGAGGCCATCCGCGGTGAGATTTTGTCCAACTTCGGCTCGCC	120
H	GTGAAGCGGAAGGGCATCGAGGCCATCCGCGGTGAGATTTTGTCCAACTTCGGCTCGCC	120
E	GTGAAGCGGAAGGGCATCGAGGCCATCCGCGGTGAGATTTTGTCCAACTTCGGCTCGCC	120

NM_001009400.2	AGTCCCCGAGCCAGGGGGACGTGCCACCCGGCCCGCTGCCCGAGGCCATACTGGCCCTT	180
H	AGTCCCCGAGCCAGGGGGACGTGCCACCCGGCCCGCTGCCCGAGGCCATACTGGCCCTT	180
E	AGTCCCCGAGCCAGGGGGACGTGCCACCCGGCCCGCTGCCCGAGGCCATACTGGCCCTT	180

NM_001009400.2	TACAACAGTACCCGCGACCGGGTGGCCGGGGAAAGTGCCGAAACGGAGCCTGAGCCAGAG	240
H	TACAACAGTACCCGCGACCGGGTGGCCGGGGAAAGTGCCGAAACGGAGCCTGAGCCAGAG	240
E	TACAACAGTACCCGCGACCGGGTGGCCGGGGAAAGTGCCGAAACGGAGCCTGAGCCAGAG	240

NM_001009400.2	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGAATACGGCAACAAAATC	300
H	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGAATACGGCAACAAAATC	300
E	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGAATACGGCAACAAAATC	300

NM_001009400.2	TATGACAAATGAAGTCTAGCTCGCACAGCATATATATGTTCTTCAACACGTCCGAGCTC	360
H	TATGACAAATGAAGTCTAGCTCGCACAGCATATATATGTTCTTCAACACGTCCGAGCTC	360
E	TATGACAAATGAAGTCTAGCTCGCACAGCATATATATGTTCTTCAACACGTCTGAGCTC	360

NM_001009400.2	CGGGAAGCAGTGCCTGAACCTGTGTTGCTCTCTC	394
H	CGGGAAGCAGTGCCTGAACCTGTGTTGCTCTCTC	394
E	CGGGAAGCAGTGCCTGAACCTGTGTTGCTCTCTC	394

Figure S3. *TGF- β* marker (394-bp) sequences and GenBank gb|NM_001009400.2| for analyzing nitrogenous bases alignment for DNA in healthy and endometritis ewes.

XM_027967477.2	CCGCGGTTGTGTAAACGGCTCCGCATCCCTCCCAGGCGCGGTCCCTAGGCCCCCGCAGCGC	60
H	CCGCGGTTGTGTAAACGGCTCCGCATCCCTCCCAGGCGCGGTCCCTAGGCCCCCGCAGCGC	60
E	CCGCGGTTGTGTAAACGGCTCCGCATCCCTCCCAGGCGCGGTCCCTAGGCCCCCGCAGCGC	60

XM_027967477.2	AGCCATGGCCTGGACGGCGGGGGCGGGCGGGCGGGTGGGACCCGCAGGGCGCTCTCGTC	120
H	AGCCATGGCCTGGACGGCGGGGGCGGGCGGGCGGGTGGGACCCGCAGGGCGCTCTCGTC	120
E	AGCCATGGCCTGGACGGCGGGGGCGGGCGGGCGGGTGGGACCCGCAGGGCGCTCTCGTC	120

XM_027967477.2	GCACACTCTGCTCTTCGAOCTGCCGCCAGCGCTGCTGGGCGAGTTCTGGCGGTCCTGGA	180
H	GCACACTCTGCTCTTCGAOCTGCCGCCAGCGCTGCTGGGCGAGTTCTGGCGGTCCTGGA	180
E	GCACACTCTGCTCTTCGAOCTGCCGCCAGCGCTGCTGGGCGAGTTCTGGCGGTCCTGGA	180

XM_027967477.2	CAGCTGCGACGGCGCGCTCGGCTGGCGCGGCCCTCGCGGAGCGGCTTTCAGCAGCTGGCT	240
H	CAGCTGCGACGGCGCGCTCGGCTGGCGCGGCCCTCGCGGAGCGGCTTTCAGCAGCTGGCT	240
E	CAGCTGCGACGGCGCGCTCGGCTGGCGCGGCCCTCGCGGAGCGGCTTTCAGCAGCTGGCT	240

XM_027967477.2	GGATGTTTCGTACATTGAAAAATATGTAGACCAAGGTAAAAGTGAACAAGAGAATTGCT	300
H	GGATGTTTCGTACATTGAAAAATATGTAGACCAAGGTAAAAGTGAACAAGAGAATTGCT	300
E	GGATGTTTCGTACATTGAAAAATATGTAGACCAAGGTAAAAGTGAACAAGAGAATTGCT	300

XM_027967477.2	TTGGTCCTGGGCTCAGAAAAACAAGACCATCGGTGACCTTTTACAGATCCTCCAGGAGAT	360
H	TTGGTCCTGGGCTCAGAAAAACAAGACCATCGGTGACCTTTTACAGATCCTCCAGGAGAT	360
E	TTGGTCCTGGGCTCAGAAAAACAAGACCATCGGTGACCTTTTACAGATCCTCCAGGAGAT	360

XM_027967477.2	GGGACATCATCGGGCTATCCATTTAATTGCAAACTATGGAGCAACCTTGAGTCCTATAGA	420
H	GGGACATCATCGGGCTATCCATTTAATTGCAAACTATGGAGCAACCTTGAGTCCTATAGA	420
E	GGGACATCATCGGGCTATCCATTTAATTGCAAACTATGGAGCAACCTTGAGTCCTATAGA	420

XM_027967477.2	GCAGAGTCATC	431
H	GCAGAGTCATC	431
E	GCAGAGTCATC	431

Figure S4. *IRAK3* marker (431-bp) sequences and GenBank gb|XM_027967477.2| for analyzing nitrogenous bases alignment for DNA in healthy and endometritis ewes.

XM_042254827.1	CAGTGGGAAGCCCAGAGTTTTTAACCACTGAACTGCCAGGGAAGTCCCCAAGAGACTGGTTT	60
H	CAGTGGGAAGCCCAGAGTTTTTAACCACTGAACTGCCAGGGAAGTCCCCAAGAGACTGGTTT	60
E	CAGTGGGAAGCCCAGAGTTTTTAACCACTGAACTGCCAGGGAAGTCCCCAAGAGACTGGTTT	60

XM_042254827.1	CTTGATCCATTTCCCTGCATATTTTTTGAATAACCCCAATGTTTATCTCCAAAGATGGAA	120
H	CTTGATCCATTTCCCTGCATATTTTTTGAATAACCCCAATGTTTATCTCCAAAGATGGAA	120
E	CTTGATCCATTTCCCTGCATATTTTTTGAATAACCCCAATGTTTATCTCCAAAGATGGAA	120

XM_042254827.1	GAGGAAGATTAAACAATAATTTGCAGAAAAGCCCTGCCTTTCCAGAGATCTAGAGTGTA	180
H	GAGGAAGATTAAACAATAATTTGCAGAAAAGCCCTGCCTTTCCAGAGATCTAGAGTGTA	180
E	GAGGAAGATTAAACAATAATTTGCAGAAAAGCCCTGCCTTTCCAGAGATCTAGAGTGTA	180

XM_042254827.1	ATGCAACCGTATGTGGTTGAGAAGTTTGAATCTTGGCTGCTTTTCGCCCTCTGCACAAGC	240
H	ATGCAACCGTATGTGGTTGAGAAGTTTGAATCTTGGCTGCTTTTCGCCCTCTGCACAAGC	240
E	ATGCAACCGTATGTGGTTGAGAAGTTTGAATCTTGGCTGCTTTTCGCCCTCTGCACAAGC	240

XM_042254827.1	AGAAACCCCGGTTTTTCGGGGACCGTGATCTCATCGTGTGCTCTCACTTTTGAAGAAAAA	300
H	AGAAACCCCGGTTTTTCGGGGACCGTGATCTCATCGTGTGCTCTCACTTTTGAAGAAAAA	300
E	AGAAACCCCGGTTTTTCGGGGACCGTGATCTCATCGTGTGCTCTCACTTTTGAAGAAAAA	300

XM_042254827.1	TAATTAATCATGGGCAAAGGAGATCCTAAGAAGCCGAGAGGCAAAATGTCATCATATGCA	360
H	TAATTAATCATGGGCAAAGGAGATCCTAAGAAGCCGAGAGGCAAAATGTCATCATATGCA	360
E	TAATTAATCATGGGCAAAGGAGATCCTAAGAAGCCGAGAGGCAAAATGTCATCATATGCA	360

XM_042254827.1	TTCTTTGTGCAAACTTGCCGGGAGGAGCACAGAAGAAGCACCCGGATGCTTCAGTCAAC	420
H	TTCTTTGTGCAAACTTGCCGGGAGGAGCACAGAAGAAGCACCCGGATGCTTCAGTCAAC	420
E	TTCTTTGTGCAAACTTGCCGGGAGGAGCACAGAAGAAGCACCCGGATGCTTCAGTCAAC	420

XM_042254827.1	TTCTCAGAGT	430
H	TTCTCAGAGT	430
E	TTCTCAGAGT	430

Figure S5. *HMGB1* marker (430-bp) sequences and GenBank gb|XM_042254827.1| for analyzing nitrogenous bases alignment for DNA in healthy and endometritis ewes.

XM_042257020.1	AGCGCGAAGCGACCTGATGGGAGTGTAGAGTGGGGAGCGGCAGCCCTATGCCTCAGCCCT	60
H	AGCGCGAAGCGACCTGATGGGAGTGTAGAGTGGGGAGCGGCAGCCCTATGCCTCAGCCCT	60
E	AGCGCGAAGCGACCTGATGGGAGTGTAGAGTGGGGAGCGGCAGCCCTATGCCTCAGCCCT	60

XM_042257020.1	CCAGTTTCCAGCGCTAACTCCAGCTGCCCTTCCAGCGCATCGGACAGCCAACTCAGCCTCA	120
H	CCAGTTTCCAGCGCTAACTCCAGCTGCCCTTCCAGCGCATCGGACAGCCAACTCAGCCTCA	120
E	CCAGTTTCCAGCGCTAACTCCAGCTGCCCTTCCAGCGCATCGGACAGCCAACTCAGCCTCA	120

XM_042257020.1	AGGTTTAAAGAAAAGAACTAGAAGGTTTCCAATCACCAGCACATCAAAAACAGAAAAGG	180
H	AGGTTTAAAGAAAAGAACTAGAAGGTTTCCAATCACCAGCACATCAAAAACAGAAAAGG	180
E	AGGTTTAAAGAAAAGAACTAGAAGGTTTCCAATCACCAGCACATCAAAAACAGAAAAGG	180

XM_042257020.1	AAAAGTCCAAGTGGATTTTATTTCTGGATTGAGATGGATCTAGAATCCCAGCTAAGCCT	240
H	AAAAGTCCAAGTGGATTTTATTTCTGGATTGAGATGGATCTAGAATCCCAGCTAAGCCT	240
E	AAAAGTCCAAGTGGATTTTATTTCTGGATTGAGATGGATCTAGAATCCCAGCTAAGCCT	240

XM_042257020.1	GGAGATCCAAAGGTCACCAGCCAGAGGGCAGGATGGAGAATGCTCATCTTCCTCCTGATG	300
H	GGAGATCCAAAGGTCACCAGCCAGAGGGCAGGATGGAGAATGCTCATCTTCCTCCTGATG	300
E	GGAGATCCAAAGGTCACCAGCCAGAGGGCAGGATGGAGAATGCTCATCTTCCTCCTGATG	300

XM_042257020.1	TGCCTGCTGCCGGCCGCCAGTGCAGTACGGGGCCACGGCTGGTGTCCGGGGAGTCTGGG	360
H	TGCCTGCTGCCGGCCGCCAGTGCAGTACGGGGCCACGGCTGGTGTCCGGGGAGTCTGGG	360
E	TGCCTGCTGCCGGCCGCCAGTGCAGTACGGGGCCACGGCTGGTGTCCGGGGAGTCTGGG	360

XM_042257020.1	GGAGCTGTGACCATCCGGTGCCGGTA 386	
H	GGAGCTGTGACCATCCGGTGCCGGTA 386	
E	GGAGCTGTGACCATCCGGTGCCGGTA 386	

Figure S6. *FCAMR* marker (386-bp) sequences and GenBank gb|XM_042257020.1| for analyzing nitrogenous bases alignment for DNA in healthy and endometritis ewes.

XM_004006435.5	AGGTCGGCTTGCTTCCTCGCGCTGGGCTGGACTGGTATAGAGGGCTTCTGAGGGCGGTGC	60
H	AGGTCGGCTTGCTTCCTCGCGCTGGGCTGGACTGGTATAGAGGGCTTCTGAGGGCGGTGC	60
E	AGGTCGGCTTGCTTCCTCGCGCTGGGCTGGACTGGTATAGAGGGCTTCTGAGGGCGGTGC	60

XM_004006435.5	GGGCGCAAGAAGCGAAGCGAGGCTGCGGAGAGCGAGCCGGGGGCTGCGGGGCTGCAGTGA	120
H	GGGCGCAAGAAGCGAAGCGAGGCTGCGGAGAGCGAGCCGGGGGCTGCGGGGCTGCAGTGA	120
E	GGGCGCAAGAAGCGAAGCGAGGCTGCGGAGAGCGAGCCGGGGGCTGCGGGGCTGCAGTGA	120

XM_004006435.5	GATGAAGCAGTGGCTCAGGGAGCGAAGACTGGCAGTGTGGCGCGACGGGCCGGCCCGGGG	180
H	GATGAAGCAGTGGCTCAGGGAGCGAAGACTGGCAGTGTGGCGCGACGGGCCGGCCCGGGG	180
E	GATGAAGCAGTGGCTCAGGGAGCGAAGACTGGCAGTGTGGCGCGACGGGCCGGCCCGGGG	180

XM_004006435.5	CCGAGGCTGCTGCTCCGGAGGCTGCTGAGACGCCCGCGCGGCCGGCGTGGAGAGCGACAG	240
H	CCGAGGCTGCTGCTCCGGAGGCTGCTGAGACGCCCGCGCGGCCGGCGTGGAGAGCGACAG	240
E	CCGAGGCTGCTGCTCCGGAGGCTGCTGAGACGCCCGCGCGGCCGGCGTGGAGAGCGACAG	240

XM_004006435.5	GCGAGAGGGAGGAGAGGCAGCGGAGCGCTGGGAAGCCGGCGGGGCGGCGGGCGGCTCGAG	300
H	GCGAGAGGGAGGAGAGGCAGCGGAGCGCTGGGAAGCCGGCGGGGCGGCGGGCGGCTCGAG	300
E	GCGAGAGGGAGGAGAGGCAGCGGAGCGCTGGGAAGCCGGCGGGGCGGCGGGCGGCTCGAG	300

XM_004006435.5	TTGGCCTCCCCGTCGGGATCCCCCGGGTGGAAACCATGCGGGTGGTCAAGTGGCTGACGG	360
H	TTGGCCTCCCCGTCGGGATCCCCCGGGTGGAAACCATGCGGGTGGTCAAGTGGCTGACGG	360
E	TTGGCCTCCCCGTCGGGATCCCCCGGGTGGAAACCATGCGGGTGGTCAAGTGGCTGACGG	360

XM_004006435.5	GGCTGCTCTACCAGCTCTCGCTCTTCATCACCAGGCTTGGGAAGTTCACCTTCCACCCCA	420
H	GGCTGCTCTACCAGCTCTCGCTCTTCATCACCAGGCTTGGGAAGTTCACCTTCCACCCCA	420
E	GGCTGCTCTACCAGCTCTCGCTCTTCATCACCAGGCTTGGGAAGTTCACCTTCCACCCCA	420

XM_004006435.5	GGCAGGAAGCCTTAGTGAGGACACTGGCCTCCTACGAAGTGGTGA	465
H	GGCAGGAAGCCTTAGTGAGGACACTGGCCTCCTACGAAGTGGTGA	465
E	GGCAGGAAGCCTTAGTGAGGACACTGGCCTCCTACGAAGTGGTGA	465

Figure S7. *ADAMTS20* marker (465-bp) sequences and GenBank gb|XM_004006435.5| for analyzing nitrogenous bases alignment for DNA in healthy and endometritis ewes.

XM_027976255.2	CGGCCTCAGCTTCCGGCTGGGCGCAGACCCCCCTCCACCCTCCCAGACACCTTCCCCTGCT	60
H	CGGCCTCAGCTTCCGGCTGGGCGCAGACCCCCCTCCACCCTCCCAGGCACCTTCCCCTGCT	60
E	CGGCCTCAGCTTCCGGCTGGGCGCAGACCCCCCTCCACCCTCCCAGACACCTTCCCCTGCT	60

XM_027976255.2	GCGGTCCCCCTTCCCGCCGCGCCTTTAACGAAGTCCTCGCCCCCACCTCCCCACTCCG	120
H	GCGGTCCCCCTTCCCGCCGCGCCTTTAACGAAGTCCTCGCCCCCACCTCCCCACTCCG	120
E	GCGGTCCCCCTTCCCGCCGCGCCTTTAACGAAGTCCTCGCCCCCACCTCCCCACTCCG	120

XM_027976255.2	CAATATTTTCTTTCGCTCGCCCTTCTCGCCTCCTCCATTGTTGTCTCACGTTTCCCACT	180
H	CAATATTTTCTTTCGCTCGCCCTTCTCGCCTCCTCCATTGTTGTCTCACGTTTCCCACT	180
E	CAATATTTTCTTTCGCTCGCCCTTCTCGCCTCCTCCATTGTTGTCTCACGTTTCCCACT	180

XM_027976255.2	CTTTGAGGAAGGATGTTGATCTGGAGAGCGAAGTGCCCCCTCTGCCTCCCAGGTACAGG	240
H	CTTTGAGGAAGGATGTTGATCTGGAGAGCGAAGTGCCCCCTCTGCCTCCCAGGTACAGG	240
E	CTTTGAGGAAGGATGTTGATCTGGAGAGCGAAGTGCCCCCTCTGCCTCCCAGGTACAGG	240

XM_027976255.2	TTTCGGGATTGCTGCTCGGGGACCAAGGATGGCAGAACGACGACAGGGTGCAAGTTGAA	300
H	TTTCGGGATTGCTGCTCGGGGACCAAGGATGGCAGAACGACGACAGGGTGCAAGTTGAA	300
E	TTTCGGGATTGCTGCTCGGGGACCAAGGATGGCAGAACGACGACAGGGTGCAAGTTGAA	300

XM_027976255.2	TTTTATATGAATGAAAAACACATTTAAAGAGAGACTAAAGTTATTTTTATCAAAAACCAG	360
H	TTTTATATGAATGAAAAACACATTTAAAGAGAGACTAAAGTTATTTTTATCAAAAACCAG	360
E	TTTTATATGAATGAAAAACACATTTAAAGAGAGACTAAAGTTATTTTTATCAAAAACCAG	360

XM_027976255.2	AGATCAAGTCTAAGAATAAGTCTGTTCAATTTTCTCTAAAATTATTAAGCTGCTTATTA	420
H	AGATCAAGTCTAAGAATAAGTCTGTTCAATTTTCTCTGAAATTATTAAGCTGCTTATTA	420
E	AGATCAAGTCTAAGAATAAGTCTGTTCAATTTTCTCTAAAATTATTAAGCTGCTTATTA	420

XM_027976255.2	TACATAATCCGAGTGCTACTAG	442
H	TACATAATCCGAGTGCTACTAG	442
E	TACATAATCCGAGTGCTACTAG	442

Figure S8. *KCNT2* marker (442-bp) sequences and GenBank gb|XM_027976255.2| for analyzing nitrogenous bases alignment for DNA in healthy and endometritis ewes.

XM_042253698.1	TCTGATCCTGAGGACTATTTCAGATGAAGCCAACACAGAGAACCCTTTATGGCACCTCTCCT	60
H	TCTGATCCTGAGGACTATTTCAGATGAAGCCAACACAGAGAACCCTTTATGGCACCTCTCCT	60
E	TCTGATCCTGAGGACTATTTCAGATGAAGCCAACACAGAGAACCCTTTATGGCACCTCTCCT	60

XM_042253698.1	CCCAGCACGCCTCGGCAGATGAAACGCGATGTCTCCAAGCACCAGAGGAATAGTGTCTGGG	120
H	CCCAGCACGCCTCGGCAGATGAAACGCGATGTCTCCAAGCACCAGAGGAATAGTGTCTGGG	120
E	CCCAGCACGCCTCGGCAGATGAAACGCGATGTCTCCAAGCACCAGAGGAACAGTGTCTGGG	120

XM_042253698.1	AGGCCCGCCGGCCGCGCGAATCTGAAAGAAAAAATGAATGTATCAAACCAACCTCCACAC	180
H	AGGCCCGCCGGCCGCGCGAATCTGAAAGAAAAAATGAATGTATCAAACCAACCTCCACAC	180
E	AGGCCCGCCGGCCGCGCGAATCTGAAAGAAAAAATGAATGTATCAAACCAACCTCCACAC	180

XM_042253698.1	AAAGACACTGGAAAACTGTGGAGAACGTGGAAGAATACAGCTATAAGCAGGAGAAAAAG	240
H	AAAGACACTGGAAAACTGTGGAGAACGTGGAAGAATACAGCTATAAGCAGGAGAAAAAG	240
E	AAAGACACTGGAAAACTGTGGAGAACATGGAAGAATACAGCTATAAGCAGGAGAAAAAG	240

XM_042253698.1	ATCCGAGCGGCTCTCAGGTCCACAGAGCGGGATCATAAGAAGAACGTGCAGTGCTCCTTC	300
H	ATCCGAGCGGCTCTCAGGTCCACAGAGCGGGATCATAAGAAGAACGTGCAGTGCTCCTTC	300
E	ATCCGAGCGGCTCTCAGGTCCACAGAGCGGGATCATAAGAAGAACGTGCAGTGCTCCTTC	300

XM_042253698.1	ATGCTGGACTCAGTGGGGGGCTCTCTGCCAAAAAGTCCATCCCGGATGTGGATCTCAAT	360
H	ATGCTGGACTCAGTGGGGGGCTCTCTGCCAAAAAGTCCATCCCGGATGTGGATCTCAAT	360
E	ATGCTGGACTCAGTGGGGGGCTCTCTGCCAAAAAGTCCATCCCGGATGTGGATCTCAAT	360

XM_042253698.1	AAGCCTTACCTCAGTCTCGGCTGCAGCAATGCTAAGCT	398
H	AAGCCTTACCTCAGTCTCGGCTGCAGCAATGCTAAGCT	398
E	AAGCCTTACCTCAGTCTCGGCTGCAGCAATGCTAAGCT	398

Figure S9. *MAP3K4* marker (398-bp) sequences and GenBank gb|XM_042253698.1| for analyzing nitrogenous bases alignment for DNA in healthy and endometritis ewes.

XM_042237057.1	ATCAAGGCATGGGACATTGGGGTGGCTACCATGAAGAAAGGGGAGATCTGTCAATTTACTG	60
H	ATCAAGGCATGGGACATTGGGGTGGCTACCATGAAGAAAGGGGAGATCTGTCAATTTACTG	60
E	ATCAAGGCATGGGACATTGGGGTGGCTACCATGAAGAAAGGGGAGATCTGTCAATTTACTG	60

XM_042237057.1	TGCAAAACCAGAATATGCATATGGCTCAGCTGGCAGTCTCCCCAAAATTCCTCGAATGCA	120
H	TGCAAAACCAGAATATGCATATGGCTCAGCTGGCAGTCTCCCCAAAATTCCTCGAATGCA	120
E	TGCAAAACCAGAATATGCATATGGCTCAGCTGGCAGTCTCCCCAAAATTCCTCGAATGCA	120

XM_042237057.1	ACTCTCTTTTTTGAGATTGAGCTCCTTGATTTCAAAGGAGAGGATTATTTGAAGATGGA	180
H	ACTCTCTTTTTTGAGATTGAGCTCCTTGATTTCAAAGGAGAGGATTATTTGAAGATGGA	180
E	ACTCTCTTTTTTGAGATTGAGCTCCTTGATTTCAAAGGAGAGGATTATTTGAAGATGGA	180

XM_042237057.1	GGTATTATTCGAAGAATCAAACGGAAAGGAGAAGGGTATTCAAACCCAAATGAGGGAGCG	240
H	GGTATTATTCGAAGAATCAAACGGAAAGGAGAAGGGTATTCAAACCCAAATGAGGGAGCG	240
E	GGTATTATTCGAAGAATCAAACGGAAAGGAGAAGGGTATTCAAACCCAAATGAGGGAGCG	240

XM_042237057.1	ACAGTAGAGATCCACCTGGAAGGCCGCTGTGGTGAAGGATGTTTGATTGCAGAGATGTG	300
H	ACAGTAGAGATCCACCTGGAAGGCCGCTGTGGTGAAGGATGTTTGATTGCAGAGATGTG	300
E	ACAGTAGAGATCCACCTGGAAGGCCGCTGTGGTGAAGGATGTTTGATTGCAGAGATGTG	300

XM_042237057.1	GGGTTTCATCGTTGGTGAAGGAGAAGACCACGACATTCGAATCGGAATCGACAAAGCCCTG	360
H	GGGTTTCATCGTTGGTGAAGGAGAAGACCACGACATTCGAATCGGAATCGACAAAGCCCTG	360
E	GGGTTTCATCGTTGGTGAAGGAGAAGACCACGACATTCGAATCGGAATCGACAAAGCCCTG	360

XM_042237057.1	GAGAAAATGCAGCGTGAGGAACAATGTAT	389
H	GAGAAAATGCAGCGTGAGGAACAATGTAT	389
E	GAGAAAATGCAGCGTGAGGAACAATGTAT	389

Figure S10. *FKBP5* marker (389-bp) sequences and GenBank gb|XM_042237057.1| for analyzing nitrogenous bases alignment for DNA in healthy and endometritis ewes.

XM_012097572.3	TAGCATAACAACCAACCGTGAGAAGAAGCAGCTCAGAAACCAGGACCAAACTGTATTCACTT	60
H	TAGCATAACAACCAACCGTGAGAAGAAGCAGCTCAGAAACCAGGACCAAACTGTATTCACTT	60
E	TAGCATAACAACCAACCGTGAGAAGAAGCAGCTCAGAAACCAGGACCAAACTGTATTCACTT	60

XM_012097572.3	TCATTAATCAGTTTCTCTGAGAAGGAAATGACATCTGGTCCTGTCTTCCTCTACATCTTG	120
H	TCATTAATCAGTTTCTCTGAGAAGGAAATGACATCTGGTCCTGTCTTCCTCTACATCTTG	120
E	TCATTAATCAGTTTCTCTGAGAAGGAAATGACATCTGGTCCTGTCTTCCTCTACATCTTG	120

XM_012097572.3	GTTTTTGAAAAATATTTCACTCCAGGCAGAGCGCAGAATGTGCCCTGCGACCTGGGCTAC	180
H	GTTTTTGAAAAATATTTCACTCCAGGCAGAGCGCAGAATGTGCCCTGCGACCTGGGCTAC	180
E	GTTTTTGAAAAATATTTCACTCCAGGCAGAGCGCAGAATGTGCCCTGCGACCTGGGCTAC	180

XM_012097572.3	TTCCCCTGCGGCAACACCACCAAGTGCTTACCTCAGCAGCTGCAATGCAACGGCGTGGAC	240
H	TTCCCCTGCGGCAACACCACCAAGTGCTTACCTCAGCAGCTGCAATGCAACGGCGTGGAC	240
E	TTCCCCTGCGGCAACACCACCAAGTGCTTACCTCAGCAGCTGCAATGCAACGGCATGGAC	240

XM_012097572.3	GACTGCGAAAACGGTGTGGACGAGGACAACCTGCGGAGACATCAACGGATGGTCTACACAA	300
H	GACTGCGAAAACGGTGTGGACGAGGACAACCTGCGGAGACATCAACGGATGGTCTACACAA	300
E	GACTGCGAAAACGGTGTGGACGAGGACAACCTGCGGAGACATCAATGGATGGTCTACACAA	300

XM_012097572.3	TTTGACAGATAATTATGGCAATAACTACAAAATGACTTCCTTGTATCCCAGTACTGTGGCA	360
H	TTTGACAGATAATTATGGCAATAACTACAAAATGACTTCCTTGTATCCCAGTACTGTGGCA	360
E	TTTGACAGATAATTATGGCAATAACTACAAAATGACTTCCTTGTATCCCAGTACTGTGGCA	360

XM_012097572.3	GAAACATCTGAATGCTTGGTCGGGTCTGCACCCCTGCAATGTATTTGCCAAGGTTTAGAG	420
H	GAAACATCTGAATGCTTGGTCGGGTCTGCACCCCTGCAATGTATTTGCCAAGGTTTAGAG	420
E	GAAACATCTGAATGCTTGGTCGGGTCTGCACCCCTGCAATGTATTTGCCAAGGTTTAGAG	420

XM_012097572.3	CTCGAGTGTGATGAG	435
H	CTCGAGTGTGATGAG	435
E	CTCGAGTGTGATGAG	435

Figure S11. *RXFP1* marker (435-bp) sequences and GenBank gb|XM_012097572.3| for analyzing nitrogenous bases alignment for DNA in healthy and endometritis ewes.

E	CTGCCTGAGGAGCTGCACACTCATCCAGGGCAGAGAAGGCTGGAACCGGGACACGAGCTC	60
XR_006060140.1	CTGCCTGAGGAGCTGCACACTCATCCAGGGCAGAGAAGGCTGGAACCGGGACACGAGCTC	60
H	CTGCCTGAGGAGCTGCACACTCATCCAGGGCAGAGAAGGCTGGAACCGGGACACGAGCTC	60

E	TAAGAGAGGCCAGCGTGAAGTGTTCATCACACCAGGGGATCTTCCTCCTTCTCGGCT	120
XR_006060140.1	TAAGAGAGGCCAGCGTGAAGTGTTCATCACACCAGGGGATCTTCCTCCTTCTCGGCT	120
H	TAAGAGAGGCCAGCGTGAAGTGTTCATCACACCAGGGGATCTTCCTCCTTCTCGGCT	120

E	TCTGATAGGTCCTGGGACGAAGGCGCTAAGCAGAATGGCTAACGCCAACTCAAACATATTT	180
XR_006060140.1	TCTGATAGGTCCTGGGACGAAGGCGCTAAGCAGAATGGCTAACGCCAACTCAAACATATTT	180
H	TCTGATAGGTCCTGGGACGAAGGCGCTAAGCAGAATGGCTAACGCCAACTCAAACATATTT	180

E	CTGAAAAGAGTTGCTGGGGACAAAGTGGAGCCGTGGGTAGGCCTCCTCGAGCTGGGTCTC	240
XR_006060140.1	CTGAAAAGAGTTGCTGGGGACAAAGTGGAGCCGTGGGTAGGCCTCCTCGAGCTGGGTCTC	240
H	CTGAAAAGAGTTGCTGGGGACAAAGTGGAGCCGTGGGTAGGCCTCCTCGAGCTGGGTCTC	240

E	TGAAGCAGGTGAGATGCAAGATAAAGCAATCGCTTTGCAGCCACCTTTGACGCACTGGGG	300
XR_006060140.1	TGAAGCAGGTGAGATGCAAGATAAAGCAATCGCTTTGCAGCCACCTTTGACGCACTGGGG	300
H	TGAAGCAGGTGAGATGCAAGATAAAGCAATCGCTTTGCAGCCACCTTTGACGCACTGGGG	300

E	ACTGAGTTGCCATTTTTTCAGTGGGCTGTTGCTGTTTTCTCACAGAAAAAAATTTTTCT	360
XR_006060140.1	ACTGAGTTGCCATTTTTTCAGTGGGCTGTTGCTGTTTTCTCACAGAAAAAGAAATTTTTCT	360
H	ACTGAGTTGCCATTTTTTCAGTGGGCTGTTGCTGTTTTCTCACAGAAAAAGAAATTTTTCT	360

E	TCAGTTGGATGGACGATTCAACAACG	385
XR_006060140.1	TCAGTTGGATGGACGATTCAACAACG	385
H	TCAGTTGGATGGACGATTCAACAACG	385

Figure S12. *SOD* marker (385-bp) sequences and GenBank gb|XR_006060140.1| for analyzing nitrogenous bases alignment for DNA in healthy and endometritis ewes.

XM_004016396.5	CTGCAGCGCCGCTCAGACACCATGGCGGACAACCGGGATCCAGCCAGCGACCAGATGAAA	60
H	CTGCAGCGCCGCTCAGACACCATGGCGGACAACCGGGATCCAGCCAGCGACCAGATGAAA	60
E	CTGCAGCGCCGCTCAGACACCATGGCGGACAACCGGGATCCAGCCAGCGACCAGATGAAA	60

XM_004016396.5	CATTGGAAGGAGCAGAGGGCCGCGCAGAAACCTGATGTCTGACCACTGGCGCCGGTAAT	120
H	CATTGGAAGGAGCAGAGGGCCGCGCAGAAACCTGATGTCTGACCACTGGCGCCGGTAAT	120
E	CATTGGAAGGAGCAGAGGGCCGCGCAGAAACCTGATGTCTGACCACTGGCGCCGGTAAT	120
	** *****	
XM_004016396.5	CCAGTAGGAGACAAACTCAATGTTCTGACGGTAGGGCCCCGAGGGCCCCCTTCTCGTCCAG	180
H	CCAGTAGGAGACAAACTCAATGTTCTGACGGTAGGGCCCCGAGGGCCCCCTTCTCGTCCAG	180
E	CCAGTAGGAGACAAACTCAATGTTCTGACGGTAGGGCCCCGAGGGCCCCCTTCTCGTCCAG	180

XM_004016396.5	GATGTGGTTTTCACTGATGAAATGGCTCACTTTGACCGGGAGAGAATTCTGAGAGAGTC	240
H	GATGTGGTTTTCACTGATGAAATGGCTCACTTTGACCGGGAGAGAATTCTGAGAGAGTC	240
E	GATGTGGTTTTCACTGATGAAATGGCTCACTTTGACCGGGAGAGAATTCTGAGAGAGTC	240

XM_004016396.5	GTGCACGCCAAAGGAGCAGGGGCTTTTGGCTACTTTGAGGTCACACATGACATTACCAGA	300
H	GTGCACGCCAAAGGAGCAGGGGCTTTTGGCTACTTTGAGGTCACACATGACATTACCAGA	300
E	GTGCATGCCAAAGGAGCAGGGGCTTTTGGCTACTTTGAGGTCACACATGACATTACCAGA	300

XM_004016396.5	TACTCCAAGGCGAAGGTGTTTGAGCATATTGGAAGAGGACGCCCATTCAGTTTCGCTTC	360
H	TACTCCAAGGCGAAGGTGTTTGAGCATATTGGAAGAGGACGCCCATTCAGTTTCGCTTC	360
E	TACTCCAAGGCGAAGGTGTTTGAGCATATTGGAAGAGGACGCCCATTCAGTTTCGCTTC	360

XM_004016396.5	TCCACTGTTGCTGGAGAATCAGGCTCAGCTGACACAG 397	
H	TCCACTGTTGCTGGAGAATCAGGCTCAGCTGACACAG 397	
E	TCCACTGTTGCTGGAGAATCAGGCTCAGCTGACACAG 397	

Figure S13. CAT marker (397-bp) sequences and GenBank gb|XM_004016396.5| for analyzing nitrogenous bases alignment for DNA in healthy and endometritis ewes.

XM_027968234.2	CTGAGGATCGTCTAGGAGAGGCGGCCAGCGAGGAGAAAAGGACACAGCGGCCGGACGTTT	60
H	CTGAGGATCGTCTAGGAGAGGCGGCCAGCGAGGAGAAAAGGACACAGCGGCCGGACGTTT	60
E	CTGAGGATCGTCTAGGAGAGGCGGCCAGCGAGGAGAAAAGGACACAGCGTCCGGACGTTT	60

XM_027968234.2	CCTTTTCCTGGAGTTTGAGTTTGTGAGAGCATGAAAATTGCTTATCTACCATGAACTGG	120
H	CCTTTTCCTGGAGTTTGAGTTTGTGAGAGCATGAAAATTGCTTATCTACCATGAACTGG	120
E	CCTTTTCCTGGAGTTTGAGTTTGTGAGAGCATGAAAATTGCTTATCTACCATGAACTGG	120

XM_027968234.2	AAGAACTTGTGTAATGAAAAAGTTTGGGGAGAAAGAAATTGGGAGACTGCCATGCCGTTCT	180
H	AAGAACTTGTGTAATGAAAAAGTTTGGGGAGAAAGAAATTGGGAGACTGCCATGCCGTTCT	180
E	AAGAACTTGTGTAATGAAAAAGTTTGGGGAGAAAGAAATTGGGAGACTACCATGCCGTTCT	180

XM_027968234.2	TTGATGTGCAGAAAAGCTGGGTGTTGACTTAGACCACTGGATGACAATCCAGAGTGCTG	240
H	TTGATGTGCAGAAAAGCTGGGTGTTGACTTAGACCACTGGATGACAATCCAGAGTGCTG	240
E	TTGATGTGCAGAAAAGCTGGGTGTTGACTTAGACCACTGGATGACAATCCAGAGTGCTG	240

XM_027968234.2	AGCAGCCTCACAGGATTCAGCCCGATGCCATGCTTTTGAGAAAGAATGGATAGAGTGTG	300
H	AGCAGCCTCACAGGATTCAGCCCGATGCCATGCTTTTGAGAAAGAATGGATAGAGTGTG	300
E	AGCAGCCTCACAGGATTCAGCCCGATGCCATGCTTTTGAGAAAGAATGGATAGAGTGTG	300

XM_027968234.2	CACATGGAATCGGTAGTATCCGAGCGGAGAGGAGTGCAAAATAGAATTTGAGGATTTCA	360
H	CACATGGAATCGGTAGTATCCGAGCGGAGAGGAGTGCAAAATAGAATTTGAGGATTTCA	360
E	CACATGGAATCGGTAGTATCCGAGCGGAGAGGAGTGCAAAATAGAATTTGAGGATTTCA	360

XM_027968234.2	GAGAATGTCTGCTTCGACAGAAAACGATGAAACGTCTGAATGCCATCAAGAGACA 415	
H	GAGAATGTCTGCTTCGACAGAAAACGATGAAACGTCTGAATGCCATCAAGAGACA 415	
E	GAGAATGTCTGCTTCGACAGAAAACGATGAAACGTCTGAATGCCATCAAGAGACA 415	

Figure S14. *NDUFS5* marker (415-bp) sequences and GenBank gb|XM_027968234.2| for analyzing nitrogenous bases alignment for DNA in healthy and endometritis ewes.

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MK630326.1    CTACGCAGCCGCGAGGATGGAGCGCCAGCAGCCCGACAGCATGCCCCAGGATTTGTCAGAG 60
H             CTACGCAGCCGCGAGGATGGAGCGCCAGCAGCCCGACAGCATGCCCCAGGATTTGTCAGAG 60
E             CTACGCAGCCGCGAGGATGGAGCGCCAGCAGCCCGACAGCATGCCCCAGGATTTGTCAGAG 60
              *****

MK630326.1    GCCCTGAAGGAGGCCACCAAGGAGGTGCACACCCAGGCGGAGAATGCCGAGTTCATGAAG 120
H             GCCCTGAAGGAGGCCACCAAGGAGGTGCACACCCAGGCGGAGAATGCTGAGTTCATGAAG 120
E             GCCCTGAAGGAGGCCACCAAGGAGGTGCACACCCAGGCGGAGAATGCCGAGTTCATGAAG 120
              *****

MK630326.1    AACTTTCAGAAGGGTGAGCTGACCCGAGAAGGTTTTAAGCTGGTGATGGCATCTTTGTAC 180
H             AACTTTCAGAAGGGTGAGCTGACCCGAGAAGGTTTTAAGCTGGTGATGGCATCTTTGTAC 180
E             AACTTTCAGAAGGGTGAGCTGACCCGAGAAGGTTTTAAGCTGGTGATGGCATCTTTGTAC 180
              *****

MK630326.1    CACATCTACGTGGCCCTGGAGGAGGAGATCGAACGCAACAAGGAGAACCCCGTCTATACT 240
H             CACATCTACGTGGCCCTGGAGGAGGAGATCGAACGCAACAAGGAGAACCCCGTCTATACT 240
E             CACATCTACGTGGCCCTGGAGGAGGAGATCGAACGCAACAAGGAGAACCCCGTCTATACT 240
              *****

MK630326.1    CCCCTCTACTTCCCAGAGGAGCTGCACCGCCGGGCGCCCTGGAGCAGGACATGGCCTTC 300
H             CCCCTCTACTTCCCAGAGGAGCTGCACCGCCGGGCGCCCTGGAGCAGGACATGGCCTTC 300
E             CCCCTCTACTTCCCAGAGGAGCTGCACCGCCGGGCGCCCTGGAGCAGGACATGGCCTTC 300
              *****

MK630326.1    TGGTACGGGCCCCGCTGGCAGGAGGCCATCCCCTACACACAGGCCACCAAGCGCTATGTT 360
H             TGGTACGGGCCCCGCTGGCAGGAGGCCATCCCCTACACACAGGCCACCAAGCGCTATGTT 360
E             TGGTACGGGCCCCGCTGGCAGGAGGCCATCCCCTACACACAGGCCACCAAGCGCTATGTT 360
              *****

MK630326.1    CAGCGACTCCAGGAGGT      377
H             CAGCGACTCCAGGAGGT      377
E             CAGCGACTCCAGGAGGT      377
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Figure S15. *HMOX1* marker (377-bp) sequences and GenBank gb|MK630326.1| for analyzing nitrogenous bases alignment for DNA in healthy and endometritis ewes.

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AF223942.1      CAGGAACCTACCAGCTGACGGGAGATGAGCTCATCTTCGCCACCAAGCAGGCCTGGCGCA 60
H               CAGGAACCTACCAGCTGACGGGAGATGAGCTCATCTTCGCCACCAAGCAGGCCTGGCGCA 60
E               CAGGAACCTACCAGCTGACGGGAGATGAGCTCATCTTCGCCACCAAGCAGGCCTGGCGCA 60
                *****

AF223942.1      ACGCCCCCGCTGCATCGGGAGGATCCAGTGGTGAACCTGCAGGTCTTTGACGCCCGGA 120
H               ACGCCCCCGCTGCATTGGGAGGATCCAGTGGTGAACCTGCAGGTCTTTGACGCCCGGA 120
E               ACGCCCCCGCTGCATCGGGAGGATCCAGTGGTGAACCTGCAGGTCTTTGACGCCCGGA 120
                *****

AF223942.1      GCTGTTCCACGGCCCAGGAAATGTTGGAACACATCTGTAGACACGTGCGTTACGCCACCA 180
H               GCTGTTCCACGGCCCAGGAAATGTTGGAACACATCTGTAGACACGTGCGTTACGCCACCA 180
E               GCTGTTCCACGGCCCAGGAAATGTTGGAACACATCTGTAGACACGTGCGTTACGCCACCA 180
                *****

AF223942.1      ACAACGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGCGATGGGAAGCATG 240
H               ACAACGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGCGATGGGAAGCATG 240
E               ACAACGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGCGATGGGAAGCATG 240
                *****

AF223942.1      ACTTCCGGGTCTGGAATGCCAGCTCATCCGCTATGCCGGCTACCAGATGCCAGATGGCA 300
H               ACTTCCGGGTCTGGAATGCCAGCTCATCCGCTATGCCGGCTACCAGATGCCAGATGGCA 300
E               ACTTCCGGGTCTGGAATGCCAGCTCATCCGCTATGCCGGCTACCAGATGCCAGATGGCA 300
                *****

AF223942.1      GCATCAGAGGGGACCCCGCCAGTGTGGAGTTCACACAGCTGTGCATCGACCTGGGCTGGA 360
H               GCATCAGAGGGGACCCCGCCAGTGTGGAGTTCACACAGCTGTGCATCGACCTGGGCTGGA 360
E               GCATCAGAGGGGACCCCGCCAGTGTGGAGTTCACACAGCTGTGCATCGACCTGGGCTGGA 360
                *****

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Figure S16. *NOS* marker (360-bp) sequences and GenBank gbAF223942.1| for analyzing nitrogenous bases alignment for DNA in healthy and endometritis ewes.